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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 9, 2003, 07:06:05 ; Search time 28 Seconds
(without alignments)
1294.381 Million cell updates/sec

Model: US-10-091-628-2
Perfect score: 1979
Sequence: 1 MRANCSSSSACFANSEBEL.....PGPMDCRALPFGVGHITSC 377

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

ched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: PIR 73:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|---------------------|
| 1 | 884 | 44.7 | 348 | 2 A49876 | Na+-dependent bile |
| 2 | 860.5 | 43.5 | 348 | 2 I38655 | ileal sodium-depen |
| 3 | 559.5 | 28.3 | 362 | 2 A41601 | Na+/taurocholate t |
| 4 | 553 | 27.9 | 349 | 2 I55601 | Na+/taurocholate co |
| 5 | 333.5 | 16.9 | 477 | 2 S01696 | gene P3 protein - |
| 6 | 325 | 16.4 | 321 | 2 E69902 | probable sodium-de |
| 7 | 301.5 | 15.2 | 305 | 2 D90031 | hypothetical prote |
| 8 | 299.5 | 15.1 | 318 | 2 A03295 | sodium/bile acid c |
| 9 | 299.5 | 15.1 | 323 | 2 B83757 | sodium-dependent t |
| 10 | 284 | 14.4 | 338 | 2 T02645 | hypothetical prote |
| 11 | 269.5 | 13.6 | 311 | 2 F83236 | probable transport |
| 12 | 266.5 | 13.5 | 315 | 2 B81168 | transporter NMB070 |
| 13 | 265.5 | 13.4 | 315 | 2 E81937 | probable transmem |
| 14 | 257.5 | 13.0 | 297 | 2 D83438 | probable transport |
| 15 | 250 | 12.6 | 297 | 2 E70482 | Na(+)-dependent tr |
| 16 | 238.5 | 12.1 | 292 | 2 S75443 | P3 protein - Synec |
| 17 | 223 | 11.3 | 207 | 2 G98166 | probable transport |
| 18 | 223 | 11.3 | 207 | 2 AH3120 | sodium bile acid s |
| 19 | 222.5 | 11.2 | 318 | 2 G81995 | probable transmem |
| 20 | 219.5 | 11.1 | 298 | 2 AF2462 | hypothetical prote |
| 21 | 180.5 | 9.1 | 182 | 2 I54222 | housekeeping prote |
| 22 | 171 | 8.6 | 460 | 2 T04579 | hypothetical prote |
| 23 | 156 | 7.9 | 379 | 2 T06610 | hypothetical prote |
| 24 | 142 | 7.2 | 344 | 2 T34981 | probable integral |
| 25 | 125 | 6.3 | 409 | 2 I40489 | hypothetical prote |
| 26 | 121.5 | 6.1 | 324 | 2 H72285 | conserved hypothet |
| 27 | 121 | 6.1 | 612 | 2 T40506 | major facilitator |
| 28 | 120 | 6.1 | 716 | 2 AB1070 | probable carbon st |
| 29 | 117 | 5.9 | 721 | 2 S56580 | carbon starvation |

ALIGNMENTS

RESULT 1

A49876
Na+-dependent bile acid transporter, ileal - golden hamster
C:Species: Mesocricetus auratus (golden hamster)
C:Date: 30-Jun-1995 #sequence_revision 30-Jun-1995-#text-change/ 05-Nov-1999
C:Accession: A49876
R.Wong, M.H.; Oelkers, P.; Craddock, A.L.; Dawson, P.A.
J. Biol. Chem. 269:1340-1347, 1994
A:Reference number: A49876; MUID:94117449; PMID:8288599
A:Accession: A49876
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-348 <WON>
A:Cross-references: GB:U02028; NID:G455032; PIDN:AAA18640.1; PID:G455033
C:Keywords: transmembrane protein

Query Match 44.7%; Score 884; DB 2; Length 348;
Best Local Similarity 46.9%; Pred. No. 2.6e-65;
Matches 164; Conservative 74; Mismatches 102; Indels 10; Gaps 4;

| | | | |
|----|-----|--|-----|
| QY | 7 | SSSACPANSS--EBELPVGLEVHGN--LELVFTVVSTVMMGLMPSLGCSSVEIRKLWSHI | 62 |
| DB | | | 62 |
| QY | 63 | RRPWGIAGVLLCQGLMPFTAYLLAISFLKPVQAIIVLNGCCPGGTISNIFFWVDGD | 122 |
| DB | | | 122 |
| QY | 123 | MDLSISMTTCTVAALGMWPLCIYLYTWSWSLQQNLITIPYONIGITLVCLTIPVAFGVV | 182 |
| DB | | | 182 |
| QY | 183 | NYRPKOSKILKIGAVGVGVLVAVAGVVLVAKGSWNSDITLLTISFIPPLIGHVTGF | 242 |
| DB | | | 242 |
| QY | 243 | LLALFTQSWORCRTISLETGAQNIQMCITMLQSLFTHLVMQLSPFLPGLFOLIDGF | 302 |
| DB | | | 302 |
| QY | 303 | LIVAAQTYKRLNKGKNGSGTEVCHTRKS--TSSRETNAPLEVNEE | 350 |
| DB | | | 350 |
| QY | 303 | ILLGAYVAYKK-----CHGKNNTLQKTDNEMEPNRSFQETNKGFPQDEK | 348 |
| DB | | | 348 |

RESULT 2

I38655
ileal sodium-dependent bile acid transporter - human
C:Species: Homo sapiens (man)
C:Date: 01-Mar-1996 #sequence_revision 01-Mar-1996 #text_change 21-Jul-2000
C:Accession: I38655

Wong, M.H.; Oelkers, P.; Dawson, P.A.
J. Biol. Chem. 272:27224-27234, 1997
A:Title: Identification of a mutation in the ileal sodium-dependent bile acid transporter
A:Reference number: 138655; MUID:96070831; PMID:7592981
A:Accession: 138655
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-348 <RES>
A:CROSS-references: EMBL:U10417; NID:G9223285; PIDN:AAC51870.1; PID:G959399
A:Experimental source: Crohn's disease patient (heterozygous)
A>Note: the wild type is shown; a form with 290-Ser was deficient in transport activity
C:Genetics:
A:Gene: SLC15-A2

Query Match 43.5%; Score 860.5; DB 2; Length 348;
Best Local Similarity 45.6%; Pred. No. 2.2e-63;
Matches 160; Conservative 68; Mismatches 104; Indels 19; Gaps 4;
QY 5 CSSSACPNASSEELPVGLEVHGNLELVFTVSTVMGLMFLSGCSVEIRKLWSHRR 64
14 CSGASCVCPSFNFI-----LSVVLSTVLTLALVNFSGMCNVEIKKFLGHKR 64
65 PNGIAGLLCQGLMPETAYLLAISFLSKPVQAIIVLIMGCCPGGTISNIFTFVWDGMD 124
65 PNGICUGFLCQGLMPLTGFLSVAFDLPLQAVVLLIGCCPGGTASNLAYWVDGMD 124
125 LSISMTCTVAALGMPLCIYLYTWSMSLOONLTIPTQNIQITLVCLTIPVAFGVYNY 184
125 LSVSMTCTLLAAGMPLCLLIYTKWVDSGSIPIVDNICTSLVALVVPVSGMFVNH 184
185 RPKOSKIILKIGAVVGVLLVAVAGVVLAKGWSNDITLITISFIPPLIGHTVGLL 244
185 KWPQAKIILKIGSAGAILVLIIVVGGILYQSAMIITGTFPPVAGYSLGFL 244
245 ALFTHQSMORCTISLETGAQNIQMCITMLQSLFTHLQVMSPLAYGLFOLIDGFLI 304
245 ARIAGLPWTRKIVAFETQNTQLCSTIVQSFTPEELNVVTFPLIYSIFQLAFAIF 304
305 VAAQYQYKRLKNGKNGSGCTEVCHTRKTSSTRNAPLEVNBEAGAITP 355
305 LGFVAYKK---CHGKNKAETPE---SKENGTEPESFYKAN---GGFQP 345

RESULT 3
A41601
Na+/taurocholate transport protein - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Feb-1997
C:Accession: A41601
Ragenbuch, B.; Stieger, B.; Foguet, M.; Luebbert, H.; Meier, P.J.
C. Natl. Acad. Sci. U.S.A. 88, 10629-10633, 1991
A:Title: Functional expression cloning and characterization of the hepatocyte Na(+)/bile
A:Reference number: A41601; MUID:92073340; PMID:1961729
A:Accession: A41601
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-362 <HAG>
A:CROSS-references: GB:M77429
C:Keywords: transmembrane protein

Query Match 28.3%; Score 559.5; DB 2; Length 362;
Best Local Similarity 37.2%; Pred. No. 1.4e-38;
Matches 133; Conservative 69; Mismatches 135; Indels 21; Gaps 9;
QY 10 ACPNASSEELPVGLEVHGNLELVFTVSTVMGLMFLSGCSVEIRKLWSHRRPWGIA 69
7 SAPFNFS---LPPGFC-HRATKALSIILVLMILLIMLSLGTCTMEFSKIKALHWPQKVI 62
70 VGLLCQGLMPLTAYLLAISFLSKPVQAIIVLIMGCCPGGTISNIFTFVWDGMDLSISM 129
63 VALVAQFGIMPLAFLGKIFHLSNIEALILICGCSPGCNLSNLTFLAMKGMNLSIVM 122
130 TTCSTVAALGMPLCIYLYT---WNSLOONLTIPTQNIQITLVCLTIPVAFGVYVNRW 186

Db 123 TTCSSFSALGMPLLLVYSGIYGDGDKK---VPYKIMLSLVILIPCTIGIVLKSKR 180
QY 187 PKOSKIILKIGAVVGVLLVAVAGVVLAKGWSNDIT---LLTISFIPPLIGHTVGLL 244
Db 181 PHYVPYILKGGMIITFLLSVAVTALSVNCGNSIMFVMTPHLLATSSLMSPFSGFLMGVIL 240
QY 245 -ALFTHQSMORC-RTISLETGAQNIQMCITMLQSLFTHLQVMSPLAYGLFOLIDGFL 302
Db 241 SALF--QLNPSCRTISMETGFQNIQLCSTILNVTFFPEVIGPLFFFPFLYIMIFQLAEG 298
QY 303 LIVAAYQYKRLKNGKNGSGCTEVCHTRKTSSTRNAPLEVNBEAGAITP 360
299 LIIIFRCYEKI-----KPPKOQTKITYKAAATEDATPAALEKGTNGNIPPLQPGP 350

RESULT 4
155601
Na+/taurocholate cotransporting polypeptide - human
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C:Accession: 155601
Ragenbuch, B.; Meier, P.J.
J. Clin. Invest. 93, 1326-1331, 1994
A:Title: Molecular cloning, chromosomal localization, and functional characterization of
A:Reference number: 155601; MUID:94179485; PMID:8132774
A:Accession: 155601
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-349 <RES>
A:CROSS-references: GB:L21893; NID:G410213; PIDN:AAA36381.1; PID:G410214
C:Genetics:
A:Gene: GDB:SLC10A1; NTCF
A:CROSS-references: GDB:344932; OMIM:182396
A:Map position: 14pter-14qter

Query Match 27.9%; Score 553; DB 2; Length 349;
Best Local Similarity 36.0%; Pred. No. 4.7e-38;
Matches 124; Conservative 77; Mismatches 109; Indels 34; Gaps 10;
QY 31 ELVFTVSTVMGLMFLSGCSVEIRKLWSHRRPWGIAVGLLQCGFLMPTAYLLAISF 90
Db 24 DLALSILVFLMFLIMLSLGTCTMEFSKIKALHWPQKGLAIALVAQYGIPLTAFVKGKF 83
QY 91 SLKPQAIIVLIMGCCPGGTISNIFTFVWDGMDLSISMTTCTVAALGMPLCIYLYT- 149
Db 84 RLKNIETALILVCGCSPGCNLSNVFSLAMKGMNLSIVMTTCTFCALGMPLLIYYSR 143
QY 150 ---WNSLOONLTIPTQNIQITLVCLTIPVAFGVYVNRWPKOSKIILKIGAVVGVLLV 207
Db 144 GIYDGLKDK---VPYKIGIVISLVILIPCTIGIVLKSRRPQYMYRVIKGGMII---ILL 197
QY 208 VAVAGVVLAKGWSNDI-----TLTISFIPPLIGHTVGLL-ALFTHQSMORC-RTIS 259
Db 198 CSVAVTVLSAINVGSIMFAMTPLLIIATSSLMPLIGLGVLSALFCLNG---RCRRIVS 255
QY 260 LETGAQNIQMCITMLQSLFTHLQVMSPLAYGLFOLIDGFLIIVAAQYKRLKNGH 319
Db 256 METGQNVQLCSTILNVAFPPEVIGPLFFFPFLYIMIFOLGEGLLIIAIFWCYE-KFKTPK 314
QY 320 GKNSGCTEVCHTRKTSSTRNAPLEVNBEAGAITP 363
Db 315 DK-----TKMIYTAATT-----ETIPGALNGTYKGEDC 344

RESULT 5
S01696
gene P3 protein - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 05-Nov-1999
C:Accession: S01696
R:Alcalay, M.; Toniolo, D.
Nucleic Acids Res. 16, 9527-9543, 1988

A:Title: CpG islands of the X chromosome are gene associated.

A:Reference number: S01696; MUID:890411548; PMID:3186440

A:Accession: S01696

A:Molecule type: DNA

A:Residues: 1-477 <ALC>

A:Cross-references: EMBL:X12458; NID:g35187; PIDN:CAA30998.1; PID:g35188

Query Match 16.9%; Score 333.5; DB 2; Length 477;
Best Local Similarity 31.5%; Pred. No. 7.6e-20;
Matches 87; Conservative 53; Mismatches 115; Indels 21; Gaps 3;
QY 12 PANSSEBELPVGLVHGNLELVFTVSTVMGLMFLSGCSVEIRKLSHRRPWIAGV 71
DB 172 PAEDTPATLSADLAHSENPILYLLPLIFVNKCSF--GCKVEVLVGLKMQSPQMLLG 229
QY 72 LQCQGLMPFTAYLLAISFLKPKVQAIKAVLIMGCCPGGTISNIFTFWVDGMDLSISMTT 131
DB 230 LQCQFLVPLAFVAKVMPKALALGLIITCSSPGGSGYFLSLLGGDVTLAISMTF 289
QY 132 CSTVAALGMPLCIYLYTWSMSLQNLTIPTQYNGITLVCLTIPVAFGVYVYWRPKSQ 191
DB 290 LSTVAATGFLPLSSAIYSKLLSIHETLHVPIISKILGTLLFTAIPIAVGLVLIKLPKFSQ 349
QY 192 IILKIGAVVGGVILL-----VAVAGVVLAKGWSNDITLLTISFFPLIGHTWG 241
DB 350 LLLQVVKPFSFVLLGGLFLAYRMGVFTLAGIRL-----PVLVGVITVPLVGLLVG 400
QY 242 FLALFTHQSMORCTISLETGAQNIQICITMLQLS 277
DB 401 YCLATCLKLPVAKQRTVSEVGVQNSLLALMLQLS 436

RESULT 6

E69902

Probable sodium-dependent transporter yocs - Bacillus subtilis

C:Species: Bacillus subtilis

C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000

C:Accession: E69902

R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
A.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall
isch, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
eger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowaka, A.; Seron
akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpstra, P.; Togononi, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A:Authors: Yoshikawa, H.F.; Zumstein, E.; Voehikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:198044033; PMID:9384377

A:Accession: E69902

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-321 <KUN>

A:Cross-references: GB:Z99114; GB:AL009126; NID:g2634230; PIDN:CAB13827.1; PID:g2634328
A:Experimental source: strain 168

C:Genetics:

A:Gene: yocs

C:Superfamily: Bacillus subtilis sodium-dependent transporter yocs

Query Match 16.4%; Score 325; DB 2; Length 321;
Best Local Similarity 27.6%; Pred. No. 2.6e-19;
Matches 84; Conservative 76; Mismatches 114; Indels 30; Gaps 12;

QY

33 VFTVVS---TVNMGLMFLSGCSVEIRKLSHRRPWIAGVLLCQGLMPPTAYLLAIS 89

DB

32 LFTWISSYITIFLGMFGNGLTQADPFKEUVRPQWVIGVIAQYITMPLVAFPLAG 91

QY

90 FSLKPKVQAIKAVLIMGCCPGGTISNIFTFWVDGMDLSISMTTCSTVAALGMPLCIYLYT 149

DB 92 LHLPAEIAVGVILVGCPCPGGTASNVTFLAKGNTALSVAVTITSLAPVVTPLLIIMLFA 151
QY 150 WWSLSLQNLTIPTQYNGITLV-CLTIPVAFGVYVYWRPKQ-SKII--LKIGAVVGGVLL 205
DB 152 KEW-----LPVSPGSLFISILQAVLFPPIIAGLIKVMFRRKQVAKAVHALPLVSVIG---- 202
QY 206 LVVAVAGVVLAKGSWN---SDITLLTISFIFPLIGHVTGFLLLALFTHQSMORCTISLET 262
DB 203 -IVAIVSAVSGNRENLLQGLLIFSVVILHNGIYLLGFLCAKLLKMDYSPQRAIAIEV 261
QY 263 GAQNIQICITMLQUSFTAELHVLQMLSPPLA-YGLFQIDGLFIIYAAQYTKRRLKNKH-G 320
DB 262 GMQN-----SGLGAALATAHFSPLSAVPSAIFSVMHNLGSGML-ATY--WSKVKKKQAG 313
QY 321 KKN 324
DB 314 SKS 317

RESULT 7

D90031

hypothetical protein SA2112 [imported] - Staphylococcus aureus (strain N315)

C:Species: Staphylococcus aureus

C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001

C:Accession: D90031

R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogel
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001

A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146

A:Accession: D90031

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-305 <KUR>

A:Cross-references: GB:BA000018; PID:g13702121; PIDN:BA843413.1; GSPDB:GN00149.
A:Experimental source: strain N315

C:Genetics:

A:Gene: SA2112

C:Superfamily: Bacillus subtilis sodium-dependent transporter yocs

Query Match 15.2%; Score 301.5; DB 2; Length 305;
Best Local Similarity 27.9%; Pred. No. 2.1e-17;
Matches 68; Conservative 60; Mismatches 101; Indels 15; Gaps 4;

QY 41 MNGLMFLSGCSVEIRKLSHRRPWIAGVLLCQGLMPPTAYLLAISFLKPKVQATAV 100

DB 41 LLGIVMLGMGLTITPNDPKVFKAPRAVIGVCLQFSIMPTLAFIAKSFHLPPDIAVGV 100

QY 101 LIMGCCPGGTISNIFTFWVDGMDLSISMTTCSTVAALGMPLCIYLYTWSLSLQNLTI 160

DB 101 ILVCCPGGTSSNVMYLAKANVALSVITTVSTLLAPFTVPALYILFANLEWLEVSFLSM 160

QY 161 PYONGITLVCLTIPVAFGV---YVYWRPKQSKIIKIGAVVGGVLLVAVAG---VV 214

DB 161 LWSVVVVV-----IPALGIVLQINRKIAEKASTALPILSVVAISLILAIWVSGSKHQI 216

QY 215 LAKGSNSDITLLTISFIFPLIGHVTGFLLLALFTHQSMORCTISLETGAQNIQICITML 274

DB 217 LTTG-----LLIFLVILHNVLYTIGYWLARLEKLDRQDKAVSIEVGMQNSGLAVSLA 271

QY 275 QLSF 278

DB 272 ALHP 275

RESULT 8

AD3295

sodium/bile acid cotransporter homolog, sbf family BMEI0346 [imported] - Brucella melitensis
C:Species: Brucella melitensis

C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002

C:Accession: AD3295

QY 270 CITMLQLSFT 279
Db 298 GFLAQKFT 307

RESULT 11
F83236
probable transporter PA3264 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: F83236
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Badian, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, L.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
Reference number: AB2950; MUID:20437337; PMID:10984043
Accession: F83236
Status: preliminary
A:Molecule type: DNA
A:Residues: 1-311 <STO>
A:Cross-references: GB:AE004091; NID:G9949388; PIDN:AAG06652.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA3264
C:Superfamily: Bacillus subtilis sodium-dependent transporter yocS

Query Match 13.6%; Score 269.5; DB 2; Length 311;
Best Local Similarity 25.7%; Pred. No. 9.2e-15;
Matches 75; Conservative 74; Mismatches 116; Indels 27; Gaps 8;

QY 32 LVFTVSTVMGLMFLSGCSVEIRKLSHRRPWGIAVGLLCOFLGMPFTAYLLAISFS 91
Db 34 LPLTAIAPLGLVNFGLTKGEDFREVARHPRIVLGVLQAVINPGLAWLLCRLLQ 93

QY 92 LKPVQIAVLINGCCPGGTISNFTFWVDGMDLSISMTTCTVAALGMPLCIYLYTWS 151
Db 94 LPAEIAVGVLVCCPGGTASNVMTLSRGDVALSVATSVTTLAPLVTALVWLLASA 153

QY 152 WSLQNLNLTIPYQIGITLV-CLTIPVAFGVYVYVYVYVYVYVYVYVYVYVYVYV 210
Db 154 W-----LPVSFAAMFLSLQVVLVPIALGLLAQRLLGRTQVAEVLPLV-SVFSIVVII 207

QY 211 AGVLAKGSWNSDITLLTISFTF-----PLIGHVTGFLALFTHQSWQRCRTSLEGA 264
Db 208 AAVVAASQARTAESGLLIMAVVLMHNGFGLLGYLTGKTGMPLAQR-----KALAEVGM 263

QY 265 QNIMQICITMLQLSFTAHLVQMLSPPLA-YGLFQIDGLFLVAAYQTYKRRL 315
Db 264 QN-----SGLGAALANAFSPLAAPVSAVPSALFSVWHNLSGSLAALF-----RRL 306

RESULT 12
B81168
transporter NMB0705 [imported] - Neisseria meningitidis (strain MC58 serogroup B)
C:Species: Neisseria meningitidis
C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C:Accession: B81168
R:Rettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Qi, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.; Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Vignani, A.
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
Reference number: AB1000; MUID:20175755; PMID:10710307
Accession: B81168
Status: preliminary
A:Molecule type: DNA
A:Residues: 1-315 <TET>
A:Cross-references: GB:AE002425; GB:AE002098; NID:G7225930; PIDN:AAFA1122.1; PID:G722593
A:Experimental source: serogroup B, strain MC58
C:Genetics:

A:Gene: NMB0705
C:Superfamily: Bacillus subtilis sodium-dependent transporter yocS

Query Match 13.5%; Score 266.5; DB 2; Length 315;
Best Local Similarity 26.6%; Pred. No. 1.6e-14;
Matches 81; Conservative 65; Mismatches 102; Indels 57; Gaps 10;

QY 41 MWGLMFLSGCSVEIRKLSHRRPWGIAVGLLCOFLGMPFTAYLLAISFSIKPQAIAY 100
Db 43 LLGIIMFGMGLTLKPSDFDILFKHPKAVIIGVIAQFAIMPATAMLKLLNLPABIAVGV 102

QY 101 LIMGCCPGGTISNFTFWVDGMDLSISMTTCTVAALGMPLCIYLYTWSLSQNLTI 160
Db 103 ILVCCPGGTASNVMTYLARGNVALSVATSVTSLISPLLP-AIFLML-----AGEMLEI 157

QY 161 PYQNGITLV-CLTIPVAFGVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYV 201
Db 158 QAAGMLMSIVKMWLLPIVLGLIVHKVLSGSKTEKLTALPLVSAIVLIIGAVVGASKG 217

QY 202 ----GVLLLVAVAGVVLAKGSWNSDITLLTISFTFPLIGHVTGFLALFTHQSWQRCRT 257
Db 218 IMESGLLIFAV-----VVLHNG-----IGYLLGFFAAKWTGLPYDAOKT 256

QY 258 ISLETGAQNIOMCITMLQLSFTAHLVQMLSPPLA-YGLFQIDGLFLVAAYQTYKRRLK 316
Db 257 LTIEVGMQNSGLAALAAAHFAAPV---AVPGALFSVWHNLSGSLA-----TYWAAKA 309

QY 317 NKHGK 321
Db 310 GKHKK 314

RESULT 13
B81937
probable transmembrane transport protein NMA0909 [imported] - Neisseria meningitidis (strain Z2491)
C:Species: Neisseria meningitidis
C>Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C:Accession: B81937
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel, N.; Holroyd, S.; Jagers, K.; Leather, S.; Moulle, S.; Mungall, K.; Quail, M.A.; Rajandream, P.; Rasmussen, S.; Rutherford, K.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Qi, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.; Science 287, 1809-1815, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
Reference number: AB1775; MUID:20222556; PMID:10761919
Accession: B81937
Status: preliminary
A:Molecule type: DNA
A:Residues: 1-315 <PAR>
A:Cross-references: GB:AL162754; GB:AL157959; NID:G7379424; PIDN:CAB84186.1; PID:G737962
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: NMA0909
C:Superfamily: Bacillus subtilis sodium-dependent transporter yocS

Query Match 13.4%; Score 265.5; DB 2; Length 315;
Best Local Similarity 25.9%; Pred. No. 2e-14;
Matches 79; Conservative 68; Mismatches 101; Indels 57; Gaps 10;

QY 41 MWGLMFLSGCSVEIRKLSHRRPWGIAVGLLCOFLGMPFTAYLLAISFSIKPQAIAY 100
Db 43 LLGIIMFGMGLTLKPSDFDILFKHPKAVIIGVIAQFAIMPATAMLKLLNLPABIAVGV 102

QY 101 LIMGCCPGGTISNFTFWVDGMDLSISMTTCTVAALGMPLCIYLYTWSLSQNLTI 160
Db 103 ILVCCPGGTASNVMTYLARGNVALSVATSVTSLISPLLP-AIFLML-----AGEMLEI 157

QY 161 PYQNGITLV-CLTIPVAFGVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYV 201
Db 158 QAAGMLMSIVKMWLLPIVLGLIVHKVLSGSKTEKLTALPLVSAIVLIIGAVVGASKG 217

QY 202 ----GVLLLVAVAGVVLAKGSWNSDITLLTISFTFPLIGHVTGFLALFTHQSWQRCRT 257
Db 218 IMESGLLIFAV-----VVLHNG-----IGYLLGFFAAKWTGLPYDAOKT 256

